

SEQUENCE LISTING

<110> EXELIXIS, INC.

<120> CDKL1 AS MODIFIER OF BRANCHING MORPHOGENESIS AND METHODS OF USE

<130> EX03-077C-PC

<150> US 60/420,554

<151> 2002-10-23

<160> 4

<170> PatentIn version 3.2

<210> 1

<211> 1178

<212> DNA

<213> Homo sapiens

<400> 1

gatccttttt aagaagattt attcctctat gatggagaag tatgaaaaaaaaa ttggaaaaat	60
tggagaagga tcctatggag ttgtttcaa atgtagaaac agggacacgg gtcagattgt	120
ggccatcaag aagtttctgg aatcagaaga tgaccctgtc ataaagaaaa ttgccttcg	180
ggaaatccga atgctcaagc aactcaagca tcccaacctt gttaacctcc tggaagtctt	240
caggagaaaa cggaggcttc acctgggttt tgaatattgt gaccacacag ttctccatga	300
gttggacaga taccaaagag gggtaccaga acatctcgta aagagcataa cttggcagac	360
actgcaagct gtaaattttt gccataaaca caattgcata catagagacg tgaagccaga	420
aaatatcctc atcacgaaac attccgtgat taagcttgt gactttggat ttgctcggt	480
tttgactgga ccgagtgact actatacaga ctacgtggct accaggtggt accgctcccc	540
tgagctgctg gtgggggaca cgcagtacgg ccccccggtg gatgtttggg caattggctg	600
tgtcttgct gagctgctgt caggagtgcc tctgtggcca ggaaaatcgg atgtggatca	660
gctgtatctg attaggaaga ccttggggga tctcattcct aggcaccagc aagtgtttag	720
cacgaatcag tacttcagtg gagtggaaaat tccagaccct gaagatatgg aaccacttga	780
attaaaattc ccaaacatct cttatcctgc cctggggctc ctaaaggggct gtctccacat	840
ggaccctact gaaaggctga catgtgaaca gctgttgcat cacccatatt ttgaaaacat	900
cagagaaaata gaggatttgg caaaaagaaca cgacaaaacca acaaggaaga ccctaagaaaa	960
gagccgaaag caccactgct ttacagaaac atccaagttg cagtacctac cccagctaac	1020
tggcagcagc atccttccag ctttggataa taagaagtac tactgtgata ccaagaaact	1080
taactaccgt tttccaaaca tttaaaggag ctaaggagag atgattttaa aaaaggaatc	1140
aatagatgct ttgaagaaaa taaaacttat acagttca	1178

<210> 2
 <211> 1175
 <212> DNA
 <213> Homo sapiens

<400> 2	
gatccattt aagaagattt attcctctat gatggagaag tatgaaaaaa ttggggaaaat	60
tggagaagga tcctatggag ttgtttcaa atgttagaaac agggacacgg gtcagattgt	120
ggccatcaag aagtttctgg aatcagaaga tgaccctgtc ataaagaaaa ttgcccttcg	180
ggaaatccga atgctcaagc aactcaagca tcccaacacctt gttaacctcc tggaaagtctt	240
caggaggaaa cggaggcttc acctgggttt tgaatattgt gaccacacag ttctccatga	300
gttggacaga taccaaagag ggttaccaga acatctcgta aagagcataa cttggcagac	360
actgcaagct gtaaattttt gccataaaaca caattgcata catagagacg tgaagccaga	420
aaatatcctc atcacgaaac attccgtat taagctttgt gactttggat ttgctcggct	480
tttgactgga ccgagtgact actatacaga ctacgtggct accaggtggt accgctcccc	540
tgagctgctg gtgggggaca cgcagtacgg ccccccggtg gatgtttggg caattggctg	600
tgtcttgct gagctgctgt caggagtgcc tctgtggcca ggaaaatcgg atgtggatca	660
gctgtatctg attaggaaga ccttggggga tctcattcct aggcaccacg aagtgtttag	720
cacgaatcag tacttcagtg gagtgaaaat tccagaccct gaagatatgg aaccacttga	780
attaaaattc ccaaacatct cttatcctgc cctggggctc ctaaagggtct gtctccacat	840
ggaccctact caaaggctga catgtgaaca gctgttgcat cacccatatt ttgaaaacat	900
cagagaaata gaggatttg caaaagaaca caacaaacca acaaggaaga ccctaagaaaa	960
gagccgaaag caccactgct ttacagaaac atccaagttt cagtagctac cccagctaac	1020
tggcagcagc atccttccag ctttggataa taagaagtac tactgtgata ccaagaaact	1080
taactaccgt tttccaaaca tttaaaggag ctaggagaca tgattttaaa aaaggaatca	1140
atagatgctt tgaagaaaaat aaaacttata cagtt	1175

<210> 3
 <211> 2982
 <212> DNA
 <213> Homo sapiens

<400> 3	
atggagctgt ccactgatac tggctggat cagaagagta atttcccgcc ttgtgactct	60
cgtgtctcca aagaagaagc ccaactccct ttcccaacac ctagcagcta cggtgcagac	120
tcctccaaacc agacttacgc acacaagtct cagtcgtaaa gagagcagca caaggaagta	180
cgtgtgtcc tgaaccatttgc ttctggcttg gatgggtggag aggagtctgg cttttgtgg	240
acaagtaccc gcattgatgc tggcactggg aacgggacgg atgataaagt cactgatcag	300

cacagacaca gaagatgcct ccaaggacc aaaggata acccggttc tgaggtgtgg	360
ggactgctgt tgcagggaaa tgtggaccgc tcaggagggg ctcctagcgc aggcgtcttg	420
ctccgcagac gcggttacag ctgcgttgc cacggcctgc ggaagttgc aaatctagca	480
ggtctgctct cccggcagca ggactcggcc cgccgcgtga gccaccattc tcggctgaag	540
atccattta agaagattt ttcctctatg atggagaagt ataaaaaat tggaaaatt	600
ggagaaggat cctatggagt tgtttcaaa ttagaaaca gggacacggg tcagattgtg	660
gccatcaaga agtttctgga atcagaagat gaccctgtca taaagaaaat tgcccttcgg	720
gaaatcccaa tgctcaaggc cccaagcccc tatgctgctg aaccttctct ctgtgaaatg	780
aaaatggtaa gaagagggaa gaaagaattt ctgccagcag tggcagaaaa agtagatgct	840
cctagcggag ttggaggtca aggacaggac agtgtcaactg tggatccc gggcagacgt	900
tctacctatg gcagaaaaca agaaaaacaa gtgagacaaa gagaaggaat catctactgc	960
tatgtggcag tttgcttcg gatttactat tttgaccagg gtgtgttgc caggaggaa	1020
gagcagtttc aggagcttgt gttggccct ttctgccata ttggctctta cttcacaggt	1080
catagaacca atgtgaggcc ttacattta ctactatcac gccccagccc cttcaagacg	1140
gctgctggta cctatgaggc aggtcttgc attcttgagt gcagttattt cctcgagag	1200
caagaacctt attgccctac tcaggcactg caacaacctc atcctattat agtccgtgg	1260
gccctagaag gaggtgggtt agaatctaag gaggacaggc atccccctcc taaggaggca	1320
cctgcatcat gtgagggatt tttaaggtct gcagtgccga agcaagctta cacccattc	1380
aaaaccagcc ctgacaaaag gcttagtgac tgtgttgcta cacccctgc ggctccccc	1440
accccactta tcatcagcag tgggtcctt gttgccatct gctccatgat tgatccagtt	1500
ccagaattcc attctgaagg cctgctagct aaggccactt caggaagtgc tggaatcctg	1560
gtatggatat ttttatgcaa tgatgcttt atttatggaa agtataattct cagaagtggaa	1620
gtgctatggg ttcgtggctc ccctggcttc aagagtgaag ctgcagccct ttgccataag	1680
tgttacagca gtgcggaccc aaagcgtgag cagcagcaag atttattgca aagagtggaa	1740
gaacaaagct tccacagtgt gaatggtgcc caggctagac ataaagggttc tccaagtccc	1800
caccagactc aggagccac ctggcctcac ccagtggatc ccacaccagg ccacaggtgg	1860
agctgcctgc cagtcctatc ccgtgcgcggc gcactcctca gtccttgggt ggtcgatggg	1920
accgggtgct gcggagcagg gggcggtct gatcgtggag gctcggccgc gcaggagccc	1980
acgcaactca agcatccaa ccttgttaac ctcctggaag tcttcaggag gaaacggagg	2040
cttcacctgg tggtaata ttgtgaccac acagttctcc atgagttgga cagataccaa	2100
agaggcatat gcaacatctt tgtgtgcact ggaagaagac ttgggtgagca cacagaggcc	2160

ttgtccaaga	aaaagaaaaaa	aggaggaggg	ggtcccttcc	tgaagtttag	ggcagccctct	2220
tgcaggatca	ccctgtttaa	aatgttggc	tgtgggctgg	aaaccacagg	tgatttgagt	2280
ctaaattctg	gagggggggc	cgcatactcg	gggggtggctg	cagctctcag	agcacttgt	2340
tgtggacag	agctgacatc	tagcgactct	ccccagaggt	gcatacatag	agacgtgaag	2400
ccagaaaata	tcctcatcac	gaaacattcc	gtgattaagc	tttgtgactt	tggatttgct	2460
cggctttga	ctggaccgag	tgactactat	acagactacg	tggctaccag	gtggtaccgc	2520
tcccctgagc	tgctggtggg	ggacacgcag	tacggccccc	cggtggatgt	ttgggcaatt	2580
ggctgtgtct	ttgctgagct	gctgtcagga	gtgcctctgt	ggccaggaaa	atcggatgt	2640
gatcagctgt	atctgattag	gaagacattg	ggggatotca	ttcctaggca	ccagcaagt	2700
tttagcacga	atcagtactt	cagtgagtg	aaaattccag	accctgaaga	tatgtccctc	2760
tgcctgtcag	taaccctgac	agagggaggc	ctgcttgctt	ctggggctgt	gaaacgctca	2820
cagatgggct	ccagcgtatc	acaggcaacc	agttggcctc	atccagacat	tgttgctgag	2880
acagcagagc	tcgatgatat	agcaatggca	cgtcaaacc	cagtgatgct	cagattcaac	2940
cgacagaaaag	aacaagagaa	atatttaagc	tatggagcat	ga		2982

<210> 4
<211> 358
<212> PRT
<213> Homo sapiens

<400> 4

Met	Met	Glu	Lys	Tyr	Glu	Lys	Ile	Gly	Lys	Ile	Gly	Glu	Gly	Ser	Tyr	
1					5				10					15		

Gly	Val	Val	Phe	Lys	Cys	Arg	Asn	Arg	Asp	Thr	Gly	Gln	Ile	Val	Ala	
													20	25	30	

Ile	Lys	Lys	Phe	Leu	Glu	Ser	Glu	Asp	Asp	Pro	Val	Ile	Lys	Lys	Ile
												35	40	45	

Ala	Leu	Arg	Glu	Ile	Arg	Met	Leu	Lys	Gln	Leu	Lys	His	Pro	Asn	Leu
						50			55			60			

Val	Asn	Leu	Leu	Glu	Val	Phe	Arg	Arg	Lys	Arg	Arg	Leu	His	Leu	Val
	65					70				75			80		

Phe	Glu	Tyr	Cys	Asp	His	Thr	Val	Leu	His	Glu	Leu	Asp	Arg	Tyr	Gln
						85				90			95		

Arg	Gly	Val	Pro	Glu	His	Leu	Val	Lys	Ser	Ile	Thr	Trp	Gln	Thr	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100

105

110

Gln Ala Val Asn Phe Cys His Lys His Asn Cys Ile His Arg Asp Val
115 120 125

Lys Pro Glu Asn Ile Leu Ile Thr Lys His Ser Val Ile Lys Leu Cys
130 135 140

Asp Phe Gly Phe Ala Arg Leu Leu Thr Gly Pro Ser Asp Tyr Tyr Thr
145 150 155 160

Asp Tyr Val Ala Thr Arg Trp Tyr Arg Ser Pro Glu Leu Leu Val Gly
165 170 175

Asp Thr Gln Tyr Gly Pro Pro Val Asp Val Trp Ala Ile Gly Cys Val
180 185 190

Phe Ala Glu Leu Leu Ser Gly Val Pro Leu Trp Pro Gly Lys Ser Asp
195 200 205

Val Asp Gln Leu Tyr Leu Ile Arg Lys Thr Leu Gly Asp Leu Ile Pro
210 215 220

Arg His Gln Gln Val Phe Ser Thr Asn Gln Tyr Phe Ser Gly Val Lys
225 230 235 240

Ile Pro Asp Pro Glu Asp Met Glu Pro Leu Glu Leu Lys Phe Pro Asn
245 250 255

Ile Ser Tyr Pro Ala Leu Gly Leu Leu Lys Gly Cys Leu His Met Asp
260 265 270

Pro Thr Glu Arg Leu Thr Cys Glu Gln Leu Leu His His Pro Tyr Phe
275 280 285

Glu Asn Ile Arg Glu Ile Glu Asp Leu Ala Lys Glu His Asp Lys Pro
290 295 300

Thr Arg Lys Thr Leu Arg Lys Ser Arg Lys His His Cys Phe Thr Glu
305 310 315 320

Thr Ser Lys Leu Gln Tyr Leu Pro Gln Leu Thr Gly Ser Ser Ile Leu
325 330 335

Pro Ala Leu Asp Asn Lys Lys Tyr Tyr Cys Asp Thr Lys Lys Leu Asn
340 345 350

Tyr Arg Phe Pro Asn Ile
355